

GenCore version 5.1.4-p5-A578
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OM nucleic - protein search, using frame_plus.np model

Run on: May 7, 2003, 15:14:59 ; Search time 33 Seconds

(without alignments)
5798.990 Million cell updates/sec

Title: US-09-965-830-1_COPY_6_3257

Perfect score: 6089

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0-UNITS-bits-START=1-END=1-MATRIX-blosum62-TRANS-humand40.cdi
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Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	5698	93.6	1083	4	US-09-343-494-1
3	5649.5	92.8	1082	4	US-09-336-643A-20
4	2461.5	40.4	1017	4	US-09-600-776-6
5	1901	31.2	1284	4	US-09-343-494-9
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14	417	6.8	1064	1	US-08-642-255-62	Sequence 62, Appl
15	410	6.8	960	4	US-09-219-849-5	Sequence 5, Appl
16	409	6.8	1065	1	US-08-642-255-72	Sequence 72, Appl
17	403.5	6.7	1065	1	US-08-642-255-80	Sequence 80, Appl
18	403.5	6.7	1065	3	US-08-642-246-16	Sequence 16, Appl
19	403.5	6.7	1065	4	US-09-451-206-16	Sequence 16, Appl
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22	399	6.6	1008	4	US-09-219-849-8	Sequence 8, Appl
23	396	6.5	1461	4	US-09-585-887-9	Sequence 9, Appl
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25	389.5	6.4	960	4	US-09-219-849-5	Sequence 5, Appl
26	387	6.4	1057	3	US-08-931-820-1	Sequence 3, Appl
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ALIGNMENTS

RESULT 1
US-09-600-776-2
Sequence 2, Application US/09600776
Patent No. 6326168
GENERAL INFORMATION:
APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
TITLE OF INVENTION: A novel potassium channel protein
FILE REFERENCE: Y9903-PCT
CURRENT APPLICATION NUMBER: US/09/600,776
CURRENT FILING DATE: 2000-07-21
PRIORITY APPLICATION NUMBER: JP P1998-011434
PRIORITY FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: JP P1998-346198
PRIORITY FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1083
TYPE: PRT
ORGANISM: Homo sapiens
US-09-600-776-2

Alignment Scores:

Pred. No.: 0
Score: 5704.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 93.68%
DB: 4
Length: 1083
Matches: 1083
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

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OY 121 CCCGTGTCTACTGCTGTGATGGCTTCTGTGATCCACAGGGGCTTCCCGGGCTGAGGTC 180
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: Patent No. 6413741
: GENERAL INFORMATION:
: APPLICANT: Jegla, Timothy J.
: APPLICANT: Wickenden, Alan
: APPLICANT: ICAgen, Incorporated
: TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subun
: FILE REFERENCE: 018512-001320US
: CURRENT APPLICATION NUMBER: US/09/343,494
: CURRENT FILING DATE: 1999-06-30
: EARLIER APPLICATION NUMBER: US 60/091,469
: EARLIER FILING DATE: 1998-07-01
: EARLIER APPLICATION NUMBER: US 60/116,621
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 1083
: TYPE: prt
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: human Elk (hek); Eag (ether a go-go)-like K+ gene)
US-09-343-494-1
US-09-343-494-1

Alignment Scores:
Pred. No.: 0 Length: 1083
Score: 5698.00 Matches: 1083
Percent Similarity: 99.91% Conservative: 1082
Best Local Similarity: 99.91% Mismatches: 1
Query Match: 93.58% Indels: 0
DB: 4 Gaps: 0

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DB	241	ThrValProTyrSerValCysValSerThrAlaArgLupProSerAlaAlaArgLysPro	260
OY	781	CCGACGGCTGTGACCTGGCCGTGGAGGTCCTTCATCCTTGACATTGTCTGATTTTC	840
DB	261	ProSerValCysAspLeuAlaValIleValaLeuPheIleLeuAspIleValLeuAspIhe	280
OY	841	CGTACACATGTGTGTCCAAATCGGGGCCAGGTGGTGTGGTGGCCCAAAGTCATTGGCTTC	900
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OY	901	CACATACGTACACACCTGGTTCCTGTGTGATGTGCATCGACAGCCGCTCCCTTGACCTGGTA	960
DB	301	HisTyrValThrThrPheLeuLeuAspValIleAlaAlaLeuProIheAspLeu	320
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DB	321	HisAlaPheLysValaIleValTyrPheGlyAlaHisLeuLeuLysThrValaArgLeuLeu	340
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OY	1081	ACAATGCTCATGACCGCTGTTCGACCTGTGCGACCTGGGTGGCTGCTGGTTCATTC	1140
DB	361	ThrLeuLeuMetAlaValaPheAlaLeuLeuAlaHisTyrValaIleCysValaTTPheTyr	380
OY	1141	ATTGGCCAGCGGAGATCGAGAGACAGCGAAATCCGAGTGGCTGAGATTGGCTGGCTGGAG	1200
DB	381	IleGlyIleArgGluIleGlnSerSerGlnSerGlnLeuProGluIleGlyTyrPheGln	400
OY	1201	GAGCTGGCCGCCCACTGGAGACTCCCTTACTACTGTGGGCGGAGGCCAGCTGTGAGGG	1260
DB	401	GluLeuAlaIleArgLeuGluThrProTyrTyrLeuValaIleArgArgProAlaGlyGly	420
OY	1261	AACAGCTCCGGCCAGAGAGACACTGTGACAGCAGCAGCAGCGCAAGGCCAAAGCGAGGCTG	1320
DB	421	AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu	440
OY	1321	GAGCTGGTGGGCGGCGCTGCTGCTGGCGAGCGCTACATCACCCTCCCTTACTTGGCACTC	1380
DB	441	GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu	460
OY	1381	ACGACGCTCACACAGCGTGGGCTTGGCAACGTGTCCGCCCAACAGGAGACCCGAAAGATC	1440
DB	461	SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle	480
OY	1441	TTTCCATCTGCACCATGTGCTATCGGCGCCCTGAGAGCAAGCGGTGGTGGGAACCTG	1500
DB	481	PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValaValaPheIleAsnVal	500
OY	1501	ACGGGCATATATCCAGCGCATGTAAAGCGCGCGCTTGTGTACACAGCGCGCACGCGCGAC	1560
DB	501	ThrAlaIleIleGlnArgMetTyrAlaIleArgPheLeuTyrHisSerArgThrArgAsp	520
OY	1561	CTGCGGACTATATCCGATCCAGTCAACGCTATCCCAAGGCCCTTACAGCAGCGCATGTGGAG	1620
DB	521	LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGln	540
OY	1621	TACTTCAGGCGCACTGGCGCGGTGAACAATGGCATCGACACACACGAGCTGCTGCAGAC	1680
DB	541	TyrPheGlnAlaThrTTPAlaValaAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer	560

QY	1661	CTCCCTGACGAGCTGCCGCGACAGACATGGCCATGACCTGGACAGAGAGGCTCGACAGT	1740
Db	561	LeuProAspGluLeuArgGalaAspDLeuAlaMetHisLeuHisLysGluValLeuGlnLeu	580
QY	1741	CCACGTGTTGAGGGGGCCAGCCGGGGGCGCTGGGGGACACTGTCTGTGGCCCTGCGGCC	1800
Db	581	ProLeuPheGlnAlaAlaSerArgGlyCysLeuArgValLeuSerLeuAlaLeuArgPro	600
QY	1801	GGCTTCGACGCGGGGAGATACCTCATCCACCCAGGCGATGGCCCTGACAGGCCCTTAC	1860
Db	601	AlaPheCysThrProGlyGluTyrLeuLeuHisGlnGlnLysPalaLeuGlnAlaLeuTyr	620
QY	1861	TTTGTCGTCTGAGCTCCATGGAGAGTCTCAAGGCTGGACCCGTGCTGGCCATTCCTTGGG	1920
Db	621	PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly	640
QY	1921	AAAGGCGACCTGATGGCTGGCTGAGCTGCCCGGGGGAGAGGAGGAAAGGCCAAAGGCC	1980
Db	641	LysGluYAspLeuIleGlyCysGluLeuProArgArgGlnGlnValValLysAlaAsnAla	660
QY	1981	GACGTGAAGGGCTGACAGTACTGCTGCTCGAGCTGGACAGAGTGGAGCTGACAGAC	2040
Db	661	AspValLysGluYLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp	680
QY	2041	AGCCTGGCGGTGATACCCGAGTGTGGCCGCGCTTCAGTGTGGCTCCGAGGAGAGCTC	2100
Db	681	SerLeuAlaLeuTyrProGluPheAlaProAlaGlyPheSerArgGlyLeuArgGlyLeu	700
QY	2101	AGCTACAACTGGGTCTGGGGAGGCTTCGAGAGTGGACAGACAGCTCCCTGAGCGGC	2160
Db	701	SerTyrAsnLeuLysAlaGlyLysSerAlaGlnValAspThrSerSerLeuSerGly	720
QY	2161	GACAAATCCCTATATGTCACAGCTGGAGAGAGAGAGACAGACAGGGGAGAGGCCCAAG	2220
Db	721	AspAsnThrLeuMetSerThrLeuGlnGlnLysGluThrAspGlyGluIleIleProThr	740
QY	2221	GTCCTCCACAGCCCAAGTATGAGCCCTCCAGCCCTCTGCTGCTGGCTGCTGACCTCC	2280
Db	741	ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProIlyAsnThrSer	760
QY	2281	TGATCCGACGTGCCAAGCTGCTATCCCACTGCAACAGACACCCGCGCTCGTCTAGCT	2340
Db	761	SerSerSerAlaAlaLysLeuLeuLeuSerProArgArgThrAlaProArgProArgLeuGly	780
QY	2341	GGCAGAGGAGCCAGGCGAGGCGAGGGGCTTTGAAAGCTGAGCTGGCCCTCTGCTCC	2400
Db	781	GlyArgGlyArgArgProGlyArgAlaGlyAlaLeuLysAlaGlnAlaGlyProSerAlaPro	800
QY	2401	CCACGGGCTTAGAGGGGCTACGGCTGCCCTATGCCATGGATGGAGTGGCCCAAGATCTG	2460
Db	801	ProAlaGlnAlaLeuGlnGluGlyLeuArgLeuProMetProThrAsnValProPhePheLeu	820
QY	2461	AGCCCCAGGAGTAGTGAATGGATTAAGAGGGCTGGCTGGACAGCCCAAGTTCTCT	2520
Db	821	SerProArgValValAspGlyIleGlnAspIlyCysLysSerAspGlnProIlyAsnThrSer	840
QY	2521	TTCCCGGTGGGCGACTGTCGGCCGGAATGTAGCAGACAGCCCTCCCTGGACCAAGAGC	2580
Db	841	PheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer	860
QY	2581	GGGCTCTACACTTCCCATGGGCGCCAGAGGCAAGAAACAGACACACTGGACAG	2640
Db	861	GlyLeuLeuThrValProHisGlyProSerGlnAlaArgAsnThrAspThrLeuAspLys	880
QY	2641	CTTCGCGAGCGGTGACAGAGCTGTACAGACAGGTGCTGACAGATGGGGAAGGACTGAG	2700
Db	881	LeuArgGlnAlaValThrGluLeuSerGlnGlnValLeuGlnMetArgGluGlyLeuGln	900
QY	2701	TCACTTCGCAAGGCTGTGACGCTTGCTCGGGGCGCCACAGGAGAGGTCGCTGCCCTCG	2760
Db	901	SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg	920
QY	2761	GCATCGGAGAGGGGCGCTGGCCAGCCAGCCACCTCCGGGCTTCTGACACTGTGTGTGTG	2820

Accession	Protein	Start	End	Score	E-value	Identical	Similar
Db	921 Alaserglygluuglyprocyproalaserthserglyleuenglnproleucysal	1	100	100	0.0	100	100
QY	2821 GACACTGGGGCATTCCTCTACTGGCTGCAGAGCCAGCTGGCTGTGTTGATGGAGCT	1	100	100	0.0	100	100
Db	941 AspThrglyAlaserSeryrcysleuenglnproProAlaIglyserValleuSerglythr	1	100	100	0.0	100	100
QY	2881 TGGCCCAACCCGTGTCGGGGGCTCCCTCCCTCATGGCAGCCCTGGCCCTGGGGCCCCA	1	100	100	0.0	100	100
Db	961 TrpProHisProAlaProIglyProProProleuMetAlaProItrpProIglyProPro	1	100	100	0.0	100	100
QY	2941 GCCTCTACAGATCCGCCCTGGCCCGAGCAGCAAGCTTCTGGACCTCCACTCAGACTCA	1	100	100	0.0	100	100
Db	981 AlaSerGlnserSerProtrpProAlaAlaThrAlaIhetrPthrSerThSerAspSer	1	100	100	0.0	100	100
QY	3001 GAGCCCCCTGACCTCAGAGAGACSTCTGCTTGAGGCCAGCAGCCCTGGCTCCCTCCCT	1	100	100	0.0	100	100
Db	1001 GluProProAlaIserglyAspIleucysSerGlnProSerThrProAlaIserProProPro	1	100	100	0.0	100	100
QY	3061 TCTGAGAGAGGGCTGAGACTGGGGCCCGCAGAGCCTGTGAGCCAGGCTGAGAGCTAC	1	100	100	0.0	100	100
Db	1021 SerGluGluGlyAlaIarGlyThrglyProAlaGlnProValSerGlnAlaGluAlaThrSer	1	100	100	0.0	100	100
QY	3121 ACTGAGAGACCCCCACAGGGGTGAGGGGGCTGGCCCTGGCCCTGGGAGCCCCACAGCCTG	1	100	100	0.0	100	100
Db	1041 ThrGlyIuIuProProProIglySerGlyGlyLeuAlaIeuProItrpAspProAlaSerIeu	1	100	100	0.0	100	100
QY	3181 GAGATGGTCTTATTGGCTGCCATGGCTGTGGCAGCATCCAGTGGAGCCAGGAAGAGGC	1	100	100	0.0	100	100
Db	1061 GluMetValIeuIleGlycysShsIglySerGlyThrValGlnItrpThrGlnGluGlyIu	1	100	100	0.0	100	100
QY	3241 ACAGGGGCTC 3249	1	100	100	0.0	100	100
Db	1081 ThrGlyVal 1083	1	100	100	0.0	100	100

RESULT 3
US-09-326

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US-09-336-643A-20
: Sequence 20, Application US/09336643A
: Patent No. 6399761
: GENERAL INFORMATION:
: APPLICANT: Miller, Andrew P.
: APPLICANT: Curran, Mark Edward
: APPLICANT: Hu, Ping
: APPLICANT: Rutter, Marc
: APPLICANT: Wang, Jian-Wang
: TITLE OF INVENTION: No. 6399761e1 Human Potassium Channels
: FILE REFERENCE: SEQ-15p
: CURRENT APPLICATION NUMBER: US/09/336,643A
: CURRENT FILING DATE: 1999-06-18
: PRIOR APPLICATION NUMBER: 60/076,687
: PRIOR FILING DATE: 1998-08-07
: PRIOR APPLICATION NUMBER: 60/116,448
: PRIOR FILING DATE: 1999-01-19
: PRIOR APPLICATION NUMBER: PCT/US99/03826
: PRIOR FILING DATE: 1999-02-22
: NUMBER OF SEQ ID NOS: 87
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 20
: LENGTH: 1062
: TYPE: PRT
: ORGANISM: H. sapiens
US-09-336-643A-20

Alignment Scores:
Pred. No.: 0
Score: 5649.50
Percent Similarity: 99.35%
Best Local Similarity: 99.35%
Query Match: 92.78%
DB: 4

Length: 1082
Matches: 1076
Conservative: 0
Mismatches: 6
Indels: 1
Gaps: 1

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OY 1141 ATTGGCCAGCGGAGATGCAGAGACGCAATCCGAGCTGCTGAGATTGGCTGGCTGCAG 1200
OY 380 IleGlyGlnArgGluIleGlnSerSerGlnSerGlnLeuProGluIleGlyTrpLeuGln 399
OY 1201 GAGCTGGCCCGCCGAGCTGAGACTCCCTACTACTGCTGGTGGCCGAGGCCAGCTGAGGG 1260
Db 400 GluLeuAlaArgArgLeuGluIrrProGlyTrpLeuValGlyArgArgProAlaGlyGly 419
OY 1261 AACAGCTCCGGCCAGAGTATACAACTGCAGACAGACAGAGGAGGCCAACAGGGAGCGGCTG 1320
Db 420 AsnSerSerGlyGlnSerAspAsnSerSerSerSerGlnAlaAsnGlyTrpGlyLeu 439
OY 1321 GAGCTGCTGGGGGGCCCGGCGGCGGAGCGGCTATCATACCTCCCTACTACTGCGACTC 1380
Db 440 GluLeuGlyGlyProSerLeuArgSerAlaArgIleThrSerLeuTrpPheAlaLeu 459
OY 1381 AGCAGCCTCAGCAGCTGGGCTTCGGCAACGTTGCCCAACACAGGACACCGAGAAATC 1440
Db 460 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGlyLysIle 479
OY 1441 TTCTCCATCTGCACATGCTCATCGGCGCTGATGCAGCGGGTGGTGTGGGAACGTG 1500
Db 480 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValAlaPheGlyAsnVal 499
OY 1501 ACGGCATATCCAGCGCATATGACGCCCGCTTCTGTGACCAACAGCCGAGCGCGAC 1560
Db 500 ThrAlaIleIleGlnArgMetGlyAlaArgArgPheLeuTrpHisSerAlaGlyTrpArgAsp 519
OY 1561 CTGCGGACTACATCCGATCCACCGATCCGATCCGAGCGCTCAAGAGCGCATGCTGAG 1620
Db 520 GlnArgAspTrpIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGln 539
OY 1621 TACTCCAGGCGCAGCTGGGGGGTGAACATGCGATGCAGACACACCGAGCTGTCAGAGC 1680
Db 540 TyrPheGlnAlaThrTrpAlaValaAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer 559
OY 1681 CTCCTGACAGCTGGCGCGAGACATCGCATCCAGCTGCACAGAGAGGTCTGACACTG 1740
Db 560 LeuProAspIleuLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 579
OY 1741 CCACTGTTTGAAGCGGCGCAGCGCGGCTGCTGCGGCGCATGTCTGCGCCCTGCGGCC 1800
Db 580 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 599
OY 1801 GCCTTGCACGCGCGGCGAGTACCTCATCCACCAAGCGATGCCGAGCGCTGTAC 1860
Db 600 AlaPheCysThrProGlyGluTrpLeuIleHisGlnIleAspAlaLeuGlnAlaLeuTrp 619
OY 1861 TTGTGCTGCTGGCTCATGAGAGTCTCAAGAGGTGCACCCGTGTCGCCATCCTAGAGG 1920
Db 620 PheValLysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 639
OY 1921 AAGGGACACTGATCGCTGAGCTGACCTCCCGCGGAGAGCAGGTGTAAAGGCCAATGCC 1980
Db 640 LysIleLysPheLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla 659
OY 1981 GAGCTGAGGGGCTGACGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
Db 660 AspAlaLysGlyLeuThrTrpCysValLeuGlnLysLeuGlnLeuAlaGlyLeuHisAsp 679
OY 2041 AGCCTTGGCTGACCCCGAATTTGCCCCCGGCTTCAGTCTGCTGCTGCTGCTGCTGCTG 2100
Db 680 SerLeuAlaLeuTrpProGluPheAlaProArgPheSerArgGlyLeuArgGlyLeuLeu 699
OY 2101 AGCTAACACCTGGGCTGGGGGGGCTGCTGACAGGTGAGACACAGCTCCTGAGCGGC 2160
Db 700 SerTrpAsnLeuGlyAlaGlyGlySerAlaGluValAspTrpSerSerLeuSerGly 719
OY 2161 GACAATACCTTATGTCACCTGAGAGAGAGACAGATGGGAGACAGGCGGCCACG 2220
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Db 720 AspAsnThrLeuMetSerThrLeuGlnGlyLysGluThrAspGlyGlnGlnIleProThr 739
OY 2221 GCTCCCCCAGCCCGACCTATAGCCCTTCAGCCCGCCCTGCTGCCCTGGCTGACCTCC 2280
Db 740 ValSerProAlaProAlaAspIleProSerSerProLeuLeuSerProLysTrpSer 759
OY 2281 TCATCCTCAGCTGCCAAGCTGCTATCCACAGCTGCACAGACACCCCGCTGCTAGGT 2340
Db 760 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProAlaGluGly 779
OY 2341 GGCAGAGGAGGCGCAGGAGGCGAGGGCTTTGAAGCTGAGGCTGGCCCTCTGCTCCC 2400
Db 780 GlyArgGlyArgProGlyLysArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 799
OY 2401 CCAAGGCGCTCAGAGGGGCTACGCGCTGCCCGCCCATCCATGAGAAATGCCCCAGATTCG 2460
Db 800 ProArgAlaLeuGlnGlyLeuArgLeuProPheProMetProTrpAsnValProProAspLeu 819
OY 2461 AGCCCGAGGTAATGATGGCATTTGAAGCGGTGTGGCTGGGACCGACCAAGTTCTCT 2520
Db 820 SerProArgValAlaAspGlyIleGlnAspGlyCysGlySerAspGlnProLysPheSer 839
OY 2521 TTCCGGGTGGCCAGTCTGGCCCGGAAATGACAGAGCCCTCCCTGGAGCCAGAGAG 2580
Db 840 PheArgValGlyIleSerGlyProGluCysSerSerSerProSerProGlyProGluSer 859
OY 2581 GGCCTGCTCACTGCTCCCATGGGCGCCAGGAGGAGCAAGAACACACACATGACACAG 2640
Db 860 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 879
OY 2641 CTTCGAGGCGGCTGACAGAGCTGTACAGACAGGTGCTGCAGATGGGGAAAGACTGCAG 2700
Db 880 LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 899
OY 2701 TCATCTGCCAGGCTGTGACAGCTTGTCCCTGCGCCCGCCACAGGGAGGGTCCGTCGCG 2760
Db 900 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGlyGlyProCysProArg 919
OY 2761 GCATCGGAGAGGGGCGCTGCCCGCCAGCAGACCTCCGCGCTTGCAGCTGTGTGTG 2820
Db 920 AlaSerGlyGlnGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuGlyVal 939
OY 2821 GACACTGGGCAATCTCTCTGCTGCTGACAGCCCGCCAGCTGCTGTGTGAGTGGAGT 2880
Db 940 AspThrGlyAlaSerSerTrpCysLeuGlnProProAlaGlySerValLeuSerGlyThr 959
OY 2881 TGGCCCACTCTGCGGGGCTCTCCCTCATGGCACCTTGCGCTGGGCTGGCCCA 2940
Db 960 TrpProHisProArgProGlyProProProLeuMetAlaProArgProTrpGlyProPro 979
OY 2941 GCGTCTCAGAGCTCCCTGCGCTGCGAGCCACACCTTTGAGACCTGACCTGAGCTCA 3000
Db 980 AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 999
OY 3001 GAGCCCGCTGCTCAGAGGACTCTGCTGAGGCCACACACCTGCTCCCTCTCTCT 3060
Db 1000 GlnProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1019
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OY 3121 ACTGGAGAGCCCGACAGAGGCTCAAGGGGCTGGGCTTGGCTGGAGCCCGACAGCTG 3180
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Db 1060 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGluGly 1079
OY 3241 ACAGGCGTC 3249
Db 1080 ThrGlyVal 1082
|||||

RESULT 4

US-09-600-776-6

Sequence 6, Application US/09600776

Patent No. 6326168

GENERAL INFORMATION:

APPLICANT: Yamamouchi Pharmaceutical Co., Ltd.

TITLE OF INVENTION: A novel potassium channel protein

FILE REFERENCE: Y9903-PCR

CURRENT APPLICATION NUMBER: US/09/600,776

CURRENT FILING DATE: 2000-07-21

PRIOR APPLICATION NUMBER: JP P1998-011434

PRIOR FILING DATE: 1998-01-23

PRIOR APPLICATION NUMBER: JP P1998-346198

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 6

LENGTH: 1017

TYPE: PRT

ORGANISM: Homo sapiens

US-09-600-776-6

Alignment Scores:

Pred. No.: 1,13e-153

Score: 2461.50

Percent Similarity: 59.19%

Best Local Similarity: 48.47%

Query Match: 40.43%

DB: 4

US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-600-776-6 (1-1017)

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Db 21 ArgPheAspGlyThrHisSerAsnPheLeuLeuAlaAsnAlaGlnGlyThrArgGlyPhe 40

QY 121 CCCGGGCTACTGCTGATGGCTCTGTGACCTACGCGGCTCTCCGGGCTAGATC 180

Db 41 ProIleValTyrCysSerAspGlyPheCysGlnLeuThrGlyTyrGlyArgThrGlyVal 60

QY 181 ATGACGGGGGCTGCTGCTCTCTCTTATGGCGACAGACACAGTGCCTGCTCCG 240

Db 61 MetGlnLysThrCysSerCysArgPheLeuTyrGlyProGlnThrSerGlnProAlaLeu 80

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QY 301 CGGAGAGCGGGCTCCCTCTGCTGCTCTGATGTGATACCATTAAGAAATGAGAA 360

Db 101 ArgLysAspGlySerAlaPheThrPysLeuLeuAspMetProIleLysAsnIleMet 120

QY 361 GGGAGGTGCTCTCTCTCTGATCTCTACAGACATCAGCAAGAAACAGAGGAGG 420

Db 121 GlyIleValValLeuPheLeuPheSerPheLysAspIleThrGlnSerGlySerProGly 140

QY 421 ---GGCCCGGACAGATGAGAGAGAGAGTGGCGCGGCGCATATGCGCGGACAGA 477

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QY 478 TCCAAAGGC-----TTCATGCGCAACCGGCGCGGAGCGCGGC 516

Db 155 SerLeuLysArgArgGlyAlaThrTrpLysPheArgSerAlaArgArgSerArgThr 174

QY 517 GTGCTTACCACTGTCCGGGCGACCTGCGAGGAGCGGAGGAGGAGGAGCAAGCTCAT 576

Db 175 ValLeuHisArgLeuThrGlnGlyHisPheGlyArgArgGlyGlnGlyMetLysAlaAsn 194

QY 577 AAGGGGTGTTTGGGGAGAAACCAACTTGCCTGATGACAAAGTAGCCGATCCGGAG 636

Db 195 AsnAsnValPheGlnProLysProSerValProGlnLysValAlaSerValGly 214

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QY 937 GCAGCGTGGCTTTGACCTGTACATGCTTACATGCTTACAGTCACTGTTCCGGCCCAT 996

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QY 997 CTGCTGAGACGCTGCGCTGCTGCGCTGCTGCGCTGCTGCGCTGCTGCGCTGCTG 1056

Db 335 LeuLeuLysThrValArgLeuLeuAlaGlnLeuAlaThrLeuLeuGlnIleAlaGly 354

QY 1057 TCGCACTACAGCGCGCTGCTGCTGACATGCTTCATGCGCTGCTGCTGCTGCTG 1116

Db 355 SerGlnCysSerAlaValValLeuThrLeuLeuMetSerValPheAlaLeuLeuAlaHis 374

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QY 1177 CTGCTGAGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1236

Db 395 LeuThrAspIleGlyTyrPheHisGlnLeuGlyLysArgLeuGlnValProTyr 412

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Db 412 ----- 412

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QY 1417 GCCAAGGAGACAGGAGAGATCTTCTCATCTGACATGCTCATGCGGCGCTGATG 1476

Db 447 AlaAsnThrAspAlaGlnLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMet 466

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QY 1597 CCCCTCAAGCAGCGCATCTGAGTACTTCCAGGCGACCTGGGCGGCTGAGCAATGGCAT 1656

Db 507 ProLeuLysGlnArgMetLeuGlnTyrPheGlnThrThrTrpAlaValAlaSerGlyIle 526

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OY 1 ATGGCGGCGCATGGGGGCTCTGGCGCTCAGAACACCTTCTGGACACCATGCTACG 60
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Db 1 MetProAlaArgLysGlyLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
61 CGCTTCACGACGCGACGACGAACTTGTCTGGCGAACGCCCGGCGGCGCTCTTC 120
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Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnGlnAlaAsnGly---Asn 39
121 CCGGTGCTACTGCTCTGATGCTGTGTGACCTCAGCGGCTCTCTCCCGGCTGAGTC 180
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Db 40 ProIleValIcysSerAspGlyPheValAspLeuThrIcysArgAlaGlnIle 59
181 ATGCACGCGGGGCTGCTGCTCTCTCTCTCTTATGGCCACAGACCATGCTGCTCCG 240
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301 CGGACAGCGGGGCTCCGCTCTGCTGTCTCTCTGATGATGATACCATTAAGATGAGAA 360
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Db 100 LysLysGlnGlyAlaProPheTyrCysLeuPheAspIleValProIleLysAsnGlnLys 119
361 GGGAGAGTGGCT 411
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411 ----- 411
Db 140 MetAsnValAsnGlnGlnLysAspSerValPheAlaLeuThrAlaAlaLeuGlnIle 159
412 -----AACGAGG 420
Db 160 ArgPheArgAlaGlySerAsnAlaGlyMetLeuGlyLeuGlyGlyLeuProGlyLeuGly 179
421 GGGCGC-----GACAGATGAGAGAGAGAGAGAGTGGCGCGCGCGAGATAGCGCG 471
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472 GCACGATCCAAAGGCTTCAATGCCAACCGCGCGGAGCGCGCGCTGCTCTACCACTG 531
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Db 200 Ala-----GlyCysAsnMetLysArgArgSerArgAlaValLeuTyrGlnLeu 216
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Db 217 SerGlnHisTyrLysProGlnLysGlyValLysThrLysLeuLysLeuGlyAsnAsn 236
583 ---GTGTTGGGAGAAACCAAACTTGCTGATGACAAAGTAGACCGCATCGCGAGAGTC 639
Db 237 PheMetHisSerThrGlnAlaProPheProGlnIcysThrGlnSerIleLysLysSer 256
640 CCCCTCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 699
Db 257 ArgLeuLeuLeuProHisTyrGlyValPheLysGlyIleTyrPaspTyrValIleLeuVal 276
700 GCCACACTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 759
Db 277 AlaThrPheTyrValAlaLeuMetValProTyrAsnAlaAlaPheAlaLysAspArg 296
760 CCGAGTCCG 819
Db 297 GlnThr-----LysValSerAspValIleValGlnAlaLeuPheIle 310
820 CTTCGACATTCCTGCTGAATTCCTGACACATTCCTGCTGCTGCTGCTGCTGCTGCTGCT 879
Db 311 ValAspIleLeuLeuAsnPheArgThrThrPheValSerArgLysGlnValValSer 330
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Db 331 AsnSerLysGlnIleAlaIleAsnTyrLeuArgGlyTyrPheAlaLeuAspLeuAla 350

OY 940 GCGGCGCCTTTCGACCTGCTACATGCTTCAAGGCTCAAGCTGTACTGGCG----- 990
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Db 369 HisIleHisLeuValLysLeuThrArgLeuLeuTyrGlnAlaArgLeuLeuGlnLysIle 388
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Db 389 AspArgTyrSerGlnHisThrAlaMetIleLeuThrLeuLeuMetPheSerPheThrLeu 408
1108 CTGCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1167
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1168 GAATCCGACGCTGCTGAG-----ATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1221
Db 427 ---TrpPheProGlnSerAsnIleGlyTyrLeuGlnLeuLeuAlaGlnArg----- 442
1222 ACTCCCTACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1281
442 ----- 442
OY 1282 AACTGACGACGACGACGACGACGACGACGACGACGCTGCTGCTGCTGCTGCTGCTGCT 1341
443 -----LysAsnAlaSerValAlaIleLeuThrThrAlaGln----- 454
OY 1342 CTGCGGACGCGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1401
Db 455 -----ThrTyrSerThrAlaLeuTyrPheThrPheThrSerLeuThrSerValGly 471
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Db 472 PheGlyAsnValSerHisAsnThrThrAlaGlnLysValPheThrIleLeuMetLeu 491
1462 ATCGGCGCCTGATGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1521
Db 492 IleGlyAlaLeuMetHisAlaValAlaPheGlyAsnValThrAlaIleIleGlnArgMet 511
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Db 512 TyrSerArgArgSerLeuTyrGlnLysTyrPArgAspLeuLysAspPheValAlaLeu 531
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Db 552 LeuSerHisGlyIleAspIleTyrGlnThrLeuArgGlnPheProGlnIleLeuArgGly 571
1702 GACATGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1761
Db 572 AspValSerMetHisLeuHisArgGlnIleLeuGlnLeuProIlePheGlnAlaIleSer 591
1762 CCGGCGCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1821
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Db 612 TyrLeuIleHisLysGlyAspAlaLeuAsnTyrIleTyrTyrLeuCysAsnGlySerMet 631
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Db 632 GlnValIleLysAspAspMetValValAlaIleLeuGlnLysGlyAspLeuValGlySer 651
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OY 2323 CCCCAGCTCTGTCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2382
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DB 933 SerGlyProSerSerProGlySerSerGlnAspGlyProGlyArGlySerSerPro 952
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DB 953 LeuArGLeuValProPheSerSerProArGProGlyGlnProGlyGlyGlnPro 972
OY 2467 AGGCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2514
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OY 2515 -----TCTCTTTC-----CGCTGAGGCGCACTCT 2538
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OY 2596 -----CCCATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2634
DB 1027 LeuSerSerProGlyArGArGProArGlyAspValGlnSerArG-----Leu 1042
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OY 2812 CTGTGTGTGACACTGGGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2871
DB 1081 ---ValThrThrProGlyProGlyProGlyProGlyProGlyProGlyProGlyPro 1099
OY 2872 AGTGGAGACTGGCCCAAGCTCTGCGGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2931
DB 1099 oleu-----ProThrLeuThrLeuAspSerLeuSerGln----- 1110
OY 2932 GGTGCCCCAGAGGTCTC-----AGAGCTCCCTGAGCTGAGAGAGAGAGAGAGAG 2982
DB 1111 -ValSerGlnPheMetAlaCysGlnGlnLeuProProGly---AlaProGlnLeuProGln 1129
OY 2983 ACCTCAGCTCAGACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3042
DB 1129 ncluglyProThrArGArGLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnPr 1149
OY 3043 CCTG 3046
DB 1149 oleu 1150
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RESULT 7
US-09-351-215-13
Sequence 13, Application US/09351215
Patent No. 6087488
GENERAL INFORMATION:
APPLICANT: Ganetzky, Barry S.
APPLICANT: Titus, Steven A.
TITLE OF INVENTION: Polynucleotides Encoding Herg-3
FILE REFERENCE: 960296, 94550
CURRENT APPLICATION NUMBER: US/09/351,215
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 08/956,242
EARLIER FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 1159
TYPE: PR
ORGANISM: Homo sapien
US-09-351-215-13

Alignment Scores:
Pred. No.: 5,93e-94 Length: 1159
Score: 1551.00 Matches: 424
Percent Similarity: 44.86 Conservative: 143
Best Local Similarity: 33.548 Mismatches: 337
Query Match: 25.478 Indels: 360
Gaps: 38

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DB 21 LysPheGlnGlyGlnSerArGlyAspPheIleIleAlaAsnAlaArgValGlnAsCys- 39
OY 121 CCGCTGCTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 40 AlaValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 59
OY 181 ATGCAAGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 60 MetGlnArGProCysThrCysAspPheLeuHIsGlyProArGThrGlnArGAlaAla 79
OY 241 CAACAGATCGCAAGAGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGlnGlnArGlyValGlnIleAlaPheTyr 99
OY 301 CGAAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 100 ArgLysAspGlySerCysPheLeuCysLeuValAspValValProValLysGlnAsp 119
OY 361 GGGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 399
DB 120 GlyAlaValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 139
OY 400 -----AGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 435
DB 140 SerProAlaHIsAspThrAsnHIsArGlyProProThrSerThrLeuAlaProGlyArg 159
OY 435 ----- 435
DB 160 AlaLysThrPheArGLeuLysLeuProAlaLeuAlaLeuThrAlaArgLysSerSer 179
OY 436 ---AAGAGACAGGTGGGTGGCGCGCGCATATGCGCGGCG---ACGATCCAAAGCTTC 489
DB 180 ValArgSerGlyGlyAlaGly-GlyAlaGlyAla-ProGlyAlaValAlaAspValAla 199
OY 490 AATGCCAACCGGCG----- 503
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OY 504 -----GCGAGCGCGCGCGCTGCTA----- 524
Db 219 sPasnHisValAlaGlyLeuGlyProAlaGluValArgAlaValAlaGlyProGlyS 239
OY 525 --CCACCTGCGCGCGCGCTGCGAGCAGCAGCCCAAGGCGAG--CAACAAGCTCAAT-- 576
Db 239 exProProArgSerAlaProGlyGlnLeu-ProSerProArgAlaHisSerLeuAsnPro 258
OY 576 ----- 576
Db 259 AspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGlySerGlyAlaSer 278
OY 577 -----AAGGCGGTGTTGGGAG 594
Db 279 ValArgAlaGlyAlaSerSerAlaAspArgGlyAlaMetArgAlaGlyValLeuProPro 298
OY 595 AAACCAAC----- 603
Db 299 ProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsnSer 318
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OY 603 ----- 603
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OY 603 ----- 603
Db 359 IleAlaProLysIleLysGluArgThrHisAsnValThrGluLysValThrGlnValLeu 378
OY 604 -----TTGCGCTAGTACAAAGTAGCCCGCCAGAGCGGCTTC 645
Db 379 SerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArgTyr 398
OY 646 ATCCGTGTCAGCTGCGCGCGCGCTGAGAGCAGCAGCTGCGGATGCTTATCTGCTGCCACA 705
Db 399 ThrIleLeuHisTyrSerProPheLysAlaValThrAspTrpLeuIleLeuLeuVal 418
OY 706 CTCTATGTCGCTGTCAGCTGCTTACAGCGTGTGTG-----AGCAGCAGCAGG 756
Db 419 IleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLysGluThrGluGln 438
OY 757 GAGCCCAAGTGC-----GCCCGCGCGCGCGCGCGCTGTCAGCTGCGC 801
Db 439 GlyProAlaThrGluLysGlyTyrAlaLysGlnProLeuAlaValAlaAspLeuIle 458
OY 802 GTGAGAGCTCTTCATCCTTGAATGTCGTAATTCCTGACACATTCGTCGTCAG 861
Db 459 ValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrValAsnAla 478
OY 862 TCGGCGCAGGCGGTGTCGCGCAAGTTCGCTGCTCCATCCATGCTACAGTCACTGTC 921
Db 479 AsnGluGluValValSerHisProGlyArgGlyLeuAlaHisTyrPheLysGlyTyrPhe 498
OY 922 CTGCTGATGTCATCAGCAGCTGCTGCTGACCTGTCAGTCAATGCTCAAGTCAAGTCA 981
Db 499 LeuIleAspMetValAlaAlaIleProPheAspLeu----- 511
OY 982 TACTTCGGGGC-----CATCTGTAAGAGCGGTGCGCTGCTGCGC 1023
Db 512 IlePheGlySerGlySerGluGluLeuIleGlyLeuLeuLysThrAlaAlaGlyLeuArg 531
OY 1024 CTGCTGCGCTGCTGCGCGCGCTGAGCGCTACTGCGAGTACAGCGCGCTGCTGACA 1083
Db 532 LeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeuPhe 551
OY 1084 CTGCTATGCGCGCTGCGCGCTGCTGCGCAGTCACTGCGCTGCGCTGCTGCTTATCAT 1143
Db 552 LeuLeuMetCysThrPheAlaLeuIleAlaHisTyrPheAlaCysIleTyrValAlaIle 571

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OY 1204 CTGCGCGCGCGCTGAGACTCCCTTACCTGCTGCGCGCGAGCGCAGCTGAGAGAG 1263
Db 589 LeuGlyAspGlnIleGlyLysProTyr-----Asn 598
OY 1264 AGCTCGCGCGCAGAGTACAACTCAGCAGCAGCAGCAGCGGCGCGCTGAG 1323
Db 599 SerSerGly----- 601
OY 1324 CTGCTGCGCGCGCGCTGCGCGCGCTGCTGATCAGTCACTGCTTACTTGCATCAGC 1383
Db 602 --LeuGlyLysProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSer 620
OY 1384 AGCTCAGCAGCTGCGCGCTGCGCAGCGCTGCGCGCAGCAGCGGAGCAGAGTCTTC 1443
Db 621 SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGlyLysIlePhe 640
OY 1444 TCCATCTGACCAATGCTATCGCGCGCTGATGTCAGCAGCGCTGCTGCTGAGAGTGA 1503
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OY 1564 CGGAGTACATCCGATCCAGCAGTATCCAGCGCGCTTACAGCAGCGCATGCTGAGTAC 1623
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OY 1624 TTCAGAGCAGCTGCGCGCTGGAACAATGCTATGCAACAGCAGCGAGCTGTCAGAGCTTC 1683
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OY 1684 CCGAGAGCTGCGCGCGCAGCATCCGATCCAGCAGCAGCAGCAGAGAGTCTGCGAG--CTG 1740
Db 721 ProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuHisCys 740
OY 1741 CCACTGTTGAGCGCGCAGCGCGAGCTGCTGCGCGCAGCTGCTGCGCGCTGCGCGCC 1800
Db 741 LysProPheArgGlyAlaThrLysGlyLeuArgAlaLeuAlaMetLysPheLysThr 760
OY 1801 GCCTTCGACGCCCGCGCGAGTACATCCAGCAGCGAGTATGCTGCGAGCGCTGTCAC 1860
Db 761 ThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAlaLeuTyr 780
OY 1861 TTGCTGCTGCTGCTGCTGATGAGGTGCTCAAGGTTGCGAGCGCTGCTGCTGCTGAGG 1920
Db 781 PheIleSerArgGlySerIleGluLeuLeuArgLysAspValAlaValAlaIleLeuGly 800
OY 1921 AAGGCGCAGTATGAGCTGTGAGTGCCTGCGCGCGGAGCAGAGTGTAAAGCGCAATGCG 1980
Db 801 LysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaAlaArgProGlyLysSerAsnGly 820
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Db 821 AspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspLeuLeuGln 840
OY 2041 AGCTTGGCTGTATCCCGGAGTTCGCGCGCTTCACTGCTGAGCTGCGAGGAGCTG 2100
Db 841 ValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu-----GluIle 858
OY 2101 AGTACAACTG-----GTGCTGCGGAGAGCTTGCAGAGTGCAG 2142
Db 859 ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerThrGluLeuGln 878
OY 2143 ACCAGTCCCTGAGCGCGCAGCAATACCTTATGTCAGCGTGGAGAGAGAGAGAGAT 2202
Db 879 GlyLysPheSerArgGlnArgLysArgLysLeuSerPheArgArgThrAspLysAsp 898

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QY 2383 GCTGGCCCTCTCTCTCCCA-----GGGCGCTAGAGGG 2418
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QY 2419 CTACGGCTG-----CCCCCATGCAATGATGCCCATGCTGAGTCCG 2466
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QY 2515 -----TCTCTTTC-----CCCTGGGCGCACTCT 2538
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QY 2596 -----CCCCATGGGCGCAGAGGAGGAGCAAGACACAGACACTCT 2634
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; APPLICANT: Keating, Mark T.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
; TITLE OF INVENTION: SYNDROME GENE
; FILE REFERENCE: 2323-136
; CURRENT APPLICATION NUMBER: US/09/226,012
; CURRENT FILING DATE: 1999-01-06
; EARLIER APPLICATION NUMBER: 09/122,847
; EARLIER FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-226-012-2
Alignment Scores:
Pred. No.: 5,93e-94 Length: 1159
Score: 1551.00 Matches: 424
Percent Similarity: 44.86% Conservative: 143
Best Local Similarity: 33.54% Mismatches: 337
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QY 435 ----- 435
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    160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer 179
QY 436 ---AAGAGACAGGTGTGGCGCGCGCGAGTATGGCCGCGG---ACGATCCAAAGCTTC 489
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    180 ValArgSerGlyGlyAlaGly-GlyAlaGlyAla-ProGlyAlaValAlaValAspValAla 199
QY 490 AATGCCAACCGGCG----- 503
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    199 sPLeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValThrAlaMeta 219
QY 504 -----GGGAGCCGCGGCGCTGCTGA----- 524
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RESULT 8
 US-09-226-012-2
 ; Sequence 2, Application US/09226012
 ; Patent No. 6207383
 ; GENERAL INFORMATION:


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QY 2263 TCCCTGCTGCACCTCCATCCTCAGCTGCCAACCTGTGATCCACAGTCAGACA 2322
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Db 902 ---ProGlyValSerAla-----LeuGlyProGlyAlaGly 914
QY 2323 CCCCCGCTGCTAGTGCAGAGGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAG 2382
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 915 AlaGlyPro-----SerSerArgGlyArgProGlyGlyProIrrpGlySerProSer 932
QY 2383 GCTGGCCCTGCTGCCCA-----CGGGCCCTAGAGGG 2418
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 933 SerGlyProSerSerProGlySerSerGluAspGlyProGlyArgSerSerPro 952
QY 2419 CTAGGCTG-----CCCCCATGCCATGGAATGCCCCCAGATCTGAGCCCC 2466
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 953 LeuArgLeuValProPheSerSerProArgProGlyGluProGlyGlyGluPro 972
QY 2467 AGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2514
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Db 973 ---LeuMetGluAspCysGlySerSerAspThrCysAsnProLeuSerGlyAlaPhe 991
QY 2515 -----TTCCTTTC-----CGCTGGGCGCACTCT 2538
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 992 SerGlyValSerAsnLeuPheSerPheTrpGlyAspSerArgGlyArgGlnTrpGlnGlu 1011
QY 2539 GGGCCGGAATGTAGACAGACCCCTCCCTGACAGAGAGAGAGAGAGAGAGAGAG 2595
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1012 LeuProArgCys-----ProAlaProThrProSerLeuLeuAsnLeuPro 1026
QY 2596 -----CCCATGGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2634
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1027 LeuSerSerProGlyArgArgProArgGlyAspValGluSerArg-----Leu 1042
QY 2635 GACAGAGCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2691
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Db 1043 AspAlaLeuGlnArgGlnLeuAsnArgLeuGlnThrArgLeuSerAlaAspMetAlaThr 1062
QY 2692 GAGCTGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2751
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Db 1063 ValLeuGlnLeuLeuGln-ArgGlnMetThrLeu----- 1073
QY 2752 TGCCCTGGGAGTGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2811
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Db 1074 -----ValProProAlaThrSerAla-- 1080
QY 2812 CTGTGTGTGACACTGGGAGATCCTCTACTGCTGACAGCCCCAGCTGCTGTCTTG 2871
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Db 1081 ---ValThrThrProGlyProGlyProThrSerThrSerProLeuLeuProValSerPr 1099
QY 2872 AGTGGAGCTTGGCCCCACCTCGTCCGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2931
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Db 1099 Oleu-----ProThrLeuThrLeuAspSerLeuSerGln-- 1110
QY 2932 GGTCCCCAGAGGCTC-----AGAGCTCCCCCTGGGCTGAGGACAGACTTTCTGG 2982
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Db 1111 -ValSerGlnPheMetAlaCysGlnGluLeuProProGly--AlaProGluLeuProGlu 1129
QY 2983 ACCTCAGCTCAGCTCAGAGAGCCCTGCTCAGAGAGAGCTCTGCTGAGCCCCAGACC 3042
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Db 1129 nGluGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnPr 1149
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Db 1149 Oleu 1150

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; FILE REFERENCE: 2323-136
; CURRENT APPLICATION NUMBER: US/09/226,012
; CURRENT FILING DATE: 1999-01-06
; EARLIER APPLICATION NUMBER: 09/122,847
; EARLIER FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1159
; TYPE: PRN
; ORGANISM: Homo sapiens
; US-09-226-012-4

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Query Match: 25.47% Indels: 360
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QY 61 CGCTTGCAGGCGACGACAGTAACTGCTGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
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Db 21 LysPheGlnGlyGlnSerArgLysPheLeuLeuAlaAsnAlaArgValGluAsnCys-- 39
QY 121 CCCGTGCTACTGCTGATAGGCTTCTGATGCTTCTGACAGGAGGAGGAGGAGGAGGAGGAG 180
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Db 40 AlaValLeuIrrCysAsnAspGlyPheCysGlnLeuGlySerArgAlaGluVal 59
QY 181 ATGCGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
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Db 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgAlaAla 79
QY 241 CAACAGATCCGCAAGGCGCTGAGACGACACAGAGATCAAGGCTGAGCTGCTGATC 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 AlaGlnLeuAlaGlnAlaLeuGlnGlyAlaGlnArgLysValGluLeuAlaPheThr 99
QY 301 CGGAAGAGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
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Db 100 ArgLysAspGlySerCysPheLeuCysLeuValAspValAlaProValLysAsnGluAsp 119
QY 361 GGGAGAGGCTCTCTCTCTA-----GTCTCTCAAGGACATC----- 399
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Db 120 GlyAlaValIleMetPheIleLeuAsnPheGluValAlaMetGlyLysAspMetValGly 139
QY 400 -----AGCAACCCAGAACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 435
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Db 140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerThrLeuAlaProGlyArg 159
QY 435 ----- 435
Db 160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer 179
QY 436 ---AAGGAGACAGGTGGGCGGCGGATATGGCGGGG---ACGATCCAAAGGCTTC 489
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 180 ValArgSerGlyGlyAlaGly-GlyAlaGlyAla-ProGlyAlaValAlaValAspVal 199
QY 490 AATGCCAACCGCG----- 503
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 199 splLeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValThrAlaMet 219
QY 504 -----GCGAGCGGCGGCTGCTA----- 524
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QY 525 ---CAACCTGCGGCGACCTGACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 576
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NAME/KEY: unsure
LOCATION: (661)
OTHER INFORMATION: Unidentified at time of filing
FEATURE:
NAME/KEY: unsure
LOCATION: (662)
OTHER INFORMATION: Unidentified at time of filing
US-08-956-242-4

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Alignment Scores:
Pred. No.: 9.18e-66
Score: 1120.50
Percent Similarity: 47.81%
Best Local Similarity: 33.59%
Query Match: 18.40%
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US-09-965-830-1_COPY_6_3257 (1-3252) x US-08-956-242-4 (1-888)

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QY 664 GCACTGAGACCACTGGGATGCTTCATCTGCTGCGCAACACTCTGTGCGCTGACT 723
DB 48 ProPheLysAlaValAlaTrpAspTrpLeuIleLeuLeuValIleTyrThrAlaIlePhe 67
QY 724 GTCCCTACAGCGTGTGTG-----AGCACAGCAGGAGAGCC 762
DB 68 ThrProTyrSerAlaIlePheLeuLeuAsnAspArgIleGlnIleGlnLysAlaArgIleCys 87
QY 763 AGTGGCGCGCGCGCGCGCGCGCTGTGACTGGCGCTGAGGTCTCTTCATCTT 822
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QY 823 GACATGTGCGAATTTCCGACACATTCGTCCAAAGTCGGCCAGGTGTGTTGCC 882
DB 108 AspIleLeuIleAsnPheThrThrTyrValAsnGlnAsnGlnIleValIleSerAsp 127
QY 883 CCAAGTCATTTGCTCCACTACAGTACACCTGTTCTCGTGGATGTCATGCGAGC 942
DB 128 ProAlaLysIleLea***HisTyrPheLysGlyTyrPheLeuIleAspMetValAla 147
QY 943 CTGCGCTTGGACCTGTACATGCTTTCAGGTCAACGTACTGTCTGCGGGCC----- 993
DB 148 IleProPheAspLeuLeu-----IlePheGlySerGlySerAsp 160
QY 994 -----CATCTGTGAAGACGTGGCGCTGCTGCGCTGCTGCGCTG 1035
DB 161 GluThrThrThrLeuIleGlyLeuLeuLysThrAlaArgLeuLeuArgValArgVal 180
QY 1036 CTTCGGGGGTGACCGGTACTGCTGACGTACAGCGCGGTGCTGACACTGTATGCC 1095
DB 181 ***ArgLysLeuAspArgTyrSerGluTyrGlyAlaValLeuMetLeuSerMetCys 200
QY 1096 GTGTTGCGCTGCTGCGGACGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1155
DB 201 IlePheAlaLeuAsnAlaHisIleThrLeuAlaCysIleThrPyrAlaIleGly----- 217
QY 1156 ATCGAGAGCAGCGAATCCAGCTGCCT-----GAGATGCGTGGCGCGCAGAG 1203
DB 218 -----AsnValGlnArgProTyrLeuThrAspLysIleGlyTyrLeuAspSer 233
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QY 1264 AGCTCGCGCAGAGTACACTGACACGACGACGAGCGGAGCGGAGCGGCGGTGAG 1323
DB 242 -----TyrAsnAspIleAspSerSer----- 249
QY 1324 CTGTGGGCGCGCGCGGTGGGCGGCGGTGCGGCGGTGCGGCGGTGCGGCGGTG 1383
DB 250 -----GlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSer 266
QY 1384 AGCTTACACAGCGTGGGCTTGGCAACGTCGCGGCAACGAGGACGAGGAGAGTCTTC 1443
DB 267 SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerIleLysIlePhe 286
QY 1444 TTCATCTGACACCATGCTATGCGCGCGCTGATGACAGCGGTCGTTGGAGCGAGAG 1503
DB 287 SerIleCysValMetLeuIleIleLysSerLeuMetTyrAlaSerIlePheGlyAsnValSer 306
QY 1504 GCGATCATCCAGCGCATGTAGCGCGCGCGCTTCTGTACACAGCGGCGGCGGCGCTG 1563
DB 307 AlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisMetGlnMetLeuArgVal 326
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DB 327 LysGluPheIleLeuArgPheHisGlnIleLeuProAsnProLeuAsnArgIleGlnIle 346
QY 1624 TTCCAGGCGACCTGGGCGGTGTAACAATGCGATGCGACACCGAGCGCTCTGACAGCTC 1683
DB 347 PheGlnHisAlaTrpThrTyrThrAsnGlyLysPheMetAsnMetValLeuLysGlyPhe 366
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QY 1741 CCACTGTTTGAAGCGCGGCGGCGGCGGCTGCTGCGGCGGCGGCGGCGGCGGCGG 1800
DB 387 LysAlaPheArgGlyAlaSerLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr 406
QY 1801 GCGTTCGACGCGCGGAGGTACTCTATCACCACAGCGGCGGCGGCGGCGGCGGCGGCTTAC 1860
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NAME/KEY: unsure
LOCATION: (662)
OTHER INFORMATION: Unidentified at time of filing
US-09-351-215-4
Alignment Scores:
Pred. No.: 9,18e-66 Length: 888
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Best Local Similarity: 33.59% Mismatches: 308
Query Match: 18,40% Indels: 169
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QY 604 TTGCTGAGTACAAAGTACGCCGATCCGGAAGTCCCTTCCTGTCAGCTGTGG 663
DB 28 LPPGGLUTYTYLSTLGLNTHRPRORGLAASNLSPHETRLLEUHLSTYRSE 47
QY 664 GCACGAGAGGACCGTGGAGGCGCTTCACGCGCGGACACGCTATGTGGCTGCTACT 723
DB 48 PPHPELYSALAVALTTPRSPTRPLEULEULEUVALILETYTHALALLEPHE 67
QY 724 GTGCCCTACAGCGTGTGTG-----AGCACAGCAGGAGGCC 762
DB 68 THRPTLYRSERIALAALAPHEULEUASNAPARGLUGLNLARGARGLUCYS 87
QY 763 AGTGGCGCGCGCGCGCGCGCGCGCGCGCTGTGACGTGGCGGAGGCTCTTCATCCTT 822
DB 88 GLYTYRSECYSSERPROLEUASNVALVALASPLEUILEVALASPILLEPHEPHELE 107
QY 823 GACATTTGCTGATTTTCCGTRACACATTCGTRCCAAAGTCGGCCAGGCTGTGCTTGGC 882
DB 108 ASPLEULEULEASNPHARGTHRTYRYVALASGLNASGLIUALVALASERASP 127
QY 883 CCAAGTCCATTTGCTGCTGCACACGTACACACGCTGCTCTGCTGATGTATCCGAGCG 942
DB 128 PROALALYSILLEALA**HISTYRPHELYSGLYTRPHELEULEASPEVVALAALA 147
QY 943 GTGCCCTTGAACCTGCTCATGCTTCAAGTCAACGCTACTTGGGGCC----- 993
DB 148 ILEPTOPHEASPLEULEU-----ILEPHEGLYSERLYSERASP 160
QY 994 -----CATCTGCTGAAGACGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1035
DB 161 GLUTHRTHTRLHLEULEGLYLEULEULSTHRLAARGLEULEUARGLEUVALARGVAL 180
QY 1036 CTTCGGCGGCTGGACCGGCTACTGCGCATACACGCGCGGTGCTGACACTGCTATGGCC 1095
DB 181 **ARGLYSLEUASPARGTYSERGLUTYRGYLAALAAVALLEUMETLEUSERMETCYS 200
QY 1096 GNTGTCGGCGCTGCGCGGACGTGGGCGCTGCGTGGTTTACATGGCCAGCGGGAG 1155
DB 201 ILEPHEALALEUASNALHISTRLPEUALACYSILETPRYALALELY----- 217
QY 1156 ATCGAGACAGCAGATCCGACGCTGCT-----GAGATGGCTGCTGACAGAG 1203
DB 218 -----ASNVALGLUARGPTOTYRLEUTHRASPLYSILLEGLYTRPLEUASPSER 233
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DB 234 LEUGLYGLINGLN-----ILEGLYLYSARG----- 241

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498 CGGCGGCGGAGCGGGCGGTCTTACCACTGTCCGGGCACCTGAG--AGCAGCC 554
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RESULT 14
US-08-642-255-62
Sequence 62, Application US/08642255
Patent No. 5773249
GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
ADDRESS: FLEHR, HOENACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 1064 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-642-255-62
Alignment Scores:
Pred. No.: 1,31e-19 Length: 1064
Score: 417.00 Matches: 308
Percent Similarity: 30.58% Conservative: 33
Best Local Similarity: 27.62% Mismatches: 476
Query Match: 6.85% Indels: 298
Gaps: 56
US-09-965-830-1_COPY_6_3257 (1-3252) x US-08-642-255-62 (1-1064)
QY 6 GGCATGGGGGCGCTCGGCGCTCAGACACCTTCTGGACACATGCTACGCGCTT 65
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Db 55 GlyProAlaGlyProProGlySer----- 62
QY 66 GCAGCGACGACAGTAACTTCTGCTGCGCAAGCCAGGTGGCGGGGCTTTCCTCCCT 125
   |||
Db 63 -----ArgGlyAspProGlyProProGlyAlaProGlyProAla 75
QY 126 GCTTACTGCTCTGATGCTTCTGTGACCTCAAGGCGCTTCTC-----CCG 170
   |||
Db 76 Gly-----ProProGlySerArgGlyAspProGlyProPro 87
QY 171 GGTAGGTATGATGACAGCGGGGCTGTGCTGCTTCTTATGGGCGCAGACAGATGA 230

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Db 280 oala-----glyProProglySerArgAspProgly-----Pr 291
OY 2612 TCCTGGGCCCCAGGAGACAGTGCAGGAGCCGCTCTGTGTCAGGGAGGAGGCTGTG 2553
Db 291 oProglyAlaProglyPro-----AlaGlyProProglySerArgAspProglyProPr 309
OY 2552 CTACATTCGGGGCCAGACTGTGCCAGCGGAGAAAGAACTGGGCTGTGCCAG-----CC 2497
Db 309 oGlyAlaProglyProAlaGlyProProglySerArgAspProglyProProglyAlaPr 339
OY 2496 ACAGCCGCTTCATACCTACTACTCTGCGGCTCAGATCTGGGGCAGCATTCATG 2437
Db 329 oGlyProAlaGlyProPro-----GlySerArgAspProglyProProglyAl 345
OY 2436 CATGGGG-----GGCAGCGGTAGCCCTCTAGGGCCCGTGGGGGAGCAGA 2392
Db 345 aProglyProAlaGlyProProglySerArgAspProglyProPro-----GlyAlaPr 363
OY 2391 GGGGCGAGCTCA-----GCCTTCAAGCCCTGTGCCCTGGGCTCCCTGTCCA-- 2340
Db 363 oGlyProAlaGlyProProglySerArgAspProglyProProglyAlaProglyProAl 383
OY 2339 -----CTAGAGAGGCGCGGGGTCTGTTCAGCTGGGGATAGCAGCTGGGAGCTGAGGA 2284
Db 383 aGlyProProglySerArgAspProglyProProglyAlaProglyProAlaGlyProPr 403
OY 2283 TGAGAGAGTGCAGCGGAGGAGCAGCAGGCGGCTGAGGGCTCATACAGCTGGGCTGGGA 2224
Db 403 oGlySerArgAspProgly-----ProProglyAla-ProG 415
OY 2223 GACCGTGGGCGCTCCCATCTGTCTCTCTCTCCAGCTGAGCATAGGGTAT 2164
Db 415 lyProAlaGlyProProglySerArgAspProglyProProgly----- 429
OY 2163 GTGCGCGCTAGGAGAGCTGTGTCACCTGTGCAGAGCTCCCGGAGCAGCTGTG 2105
Db 430 -----AlaProglyProAlaGlyProProglySerArgAspProglyProProglyAlaPr 448
OY 2104 -----AGCTAGCTCCCTCGAGGCGCAGCTGAAAGCGGCGGCAAACTCGGGGTACAG 2050
Db 448 roGlyProAlaGlyProProglySerArgAspProglyProProglyAlaGlyProAl 468
OY 2049 CCGAAGGCTGTGTCAGGCGCAGCAGCTGCAGACACTGCAGGAGCAGTACCTACGCC 1990
Db 468 laGlyProlyselAlaGlyProAlaGlyProlyselAlaGlyProlyselAlaGlyPro 488
OY 1989 CTTCAGCTGGCATTTGGCTTTA-----CCACCTGCTCCGCGGGGAGCTC 1942
Db 488 rolyselAlaGlyProAlaGlyProlyselAlaGlyProAlaGlyProProProG 508
OY 1941 ACAGCGCATCA-----GCTCGCCCTTCCTAGAGTGGCAGCAGCGTCCAC 1894
Db 508 lySerArgAspProglyProProglyAlaProgly-----P 520
OY 1893 CTTCAGCAGCTTCATGAGCAGCAGC-----AGACAAATGAGAGGCTTCAGAGGC 1843
Db 520 roAlaGlyProProglySerArgAspProglyProProglyAlaProglyProAlaGlyPr 540
OY 1842 ATGCGCTTGGTGAAGTACTGCGCGGCTGCAGAAAGCGGCGCAGGAGGAGGA 1783
Db 540 roPro-----GlySerArgAspProglyProProglyAlaProglyProAlaG 556
OY 1782 CAGTGCAGCGCAGGAGCGGCGGCTGCTCAAAAGTGCAGCTGCAGAGCTCTCT 1723
Db 556 lyProProglySerArgAspProglyProProglyAlaProglyProAlaGlyProPro 575
OY 1722 GTGCAAGTGCATGCTGTGCGCAGAGCTGTGAGGAGCTGTGCAGCAGCTCGGT 1663
Db 576 -----GlySerArgAspProgly----- 581
OY 1662 GGCTGCATGCCATTTGTTACCGCGCCAGTGGCTTGA-----AGTACTCCAGCATGCG 1609
Db 1662 ----- 1609

Db 582 -----ProProglyAlaProglyProAlaGlyProProglySerA 595
OY 1608 CTGCTTGAAGGGCTTTGGGGAATACGCTGATGCGGATGATGCGGAGCTGCGCGTGGC 1549
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OY 1548 GCTGTGTACAGAAAGCGGGGCTGATACGCTGTGATGATGCGCTCAGCTCCAAA 1489
Db 615 ly-----ProProglyAlaProglyProAlaGlyProProglySerArgAspProG 632
OY 1488 CACACCGCGCTGCATCAGGCGCGGATGACAGATGCTGACATGAGCAAGATCTTCGGT 1429
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OY 1428 GTCCGTGTGGCGACAGCTTGCAGAACCCAGCTGTGTAGGCTGTGTAGTGCAGAACTA 1369
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Db 649 -----GlyProProglyAlaProglyPro----- 656
OY 1308 GTTGGCTGCTGTGCTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1249
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OY 1248 CCTCGGCCACAGTAGTAGTAGAG-----TTCAGTGCAGGCGCGGCTGCTGAGCCA 1192
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OY 1191 GCAATTCAGAGCAGCTGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1156
Db 676 roProgly-----SerArgAspProglyProProglyAlaProG 689
OY 1155 CTCCGCTGGCCAAATGTAAACAGACAGCAGCAGCAGCTGCGGAGCAGGCGGAGAC 1096
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Db 744 -----AlaGly-----ProProglySerA 750
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OY 855 CAGCAATGTGTAGCAATTCAGCAATGTCAAGATGAAAGAGAGCTCCAGCGCAG 796
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OY 741 ACACAGCTGTAGGCGCAGTGCAGCAGCAGATAGAGTGTGGGAGCAGAGATGAAACCAATC 682
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OY 681 CCAGGT-----GGCTCAGTGCAGCAGTGCAGCAGTGCAGCAGTGCAGCAGTGCAGT 628
Db 789 ProglyAlaProglyProAlaGlyProProglySerArgAspProgly-----ProPro 806
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Db 807 Gly----- 807

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QY 567 GTGCTGGCCCTTGCGCTCTCTGACAGTGCCGAGACAGTGAGACACGCG----- 514
Db 808 -----AlaProGlyProAlaGlyProProGlySerArg 818
QY 513 ---CCGGCTCCGCG-----CCGGTGCCATTGAAGCCTTGAGTCGTGCCG 469
Db 819 AspProGlyProProGlyAlaProGlyProAlaGly-----Pro 831
QY 468 GCCATATCGCGCGCGCGCA---CCACCTGTCTCCATCTGTGGGGCCCCCTGCGTT 412
Db 832 -ProGlySerArgAspProGlyProProGlyAlaProGlyProAlaGlyProPro-GlyS 851
QY 411 CTGTGTTTGGCTGATGTCCTGTGTGAGAGACTGAGAGAGCA----- 368
Db 851 er-----ArgAspProGlyProProGlyAlaP 860
QY 367 -----CCTCCCTTCTCATCTTATGGGTATCATCATCCAGAGACCA 322
Db 860 roGlyProAlaGlyProProGlySerArgAsp-----ProGlyProProG 875
QY 321 GACGGGAGCGCCGCTCTCCGTACAGATCAGCTCAGCCTTGAACCTTGTGCTCGTC 262
Db 875 lYAlaProGlyProAlaGlyProProGlySerArgAspProGlyProProGlyAla---P 894
QY 261 CAGGGCTTCGCGATCTGTGGCGAGACCTCAGTGTGTGGCCCATAAAGAGAGA 202
Db 894 roGlyProAlaGlyProProGlySerArg----- 903
QY 201 GCAGGCACAGCCCGCTGCATGACCTCAGCCCGGAGAGCCCGTAGAGTCCAGAAAGCC 142
Db 904 --AspProGlyProProGlyAlaProGlyProAlaGlyProPro---GlySerArgAsp 922
QY 141 ATCAGACAGTAGACACAGCGGAGAGCCCGCCACCTGGGCGTTGCCACAGCAAGCTT 82
Db 922 roGlyProProGlyAlaProGlyProAlaGlyProProGly----- 935
QY 81 ACTGTGCGTCCGTCGAGAGCGCGTAGCGATGATGTCCAGAAAGGTCTGAGGCGCCAG 22
Db 936 -----SerArgAspProG 940
QY 21 GA-----GGCCCGCATGGCGG 5
Db 940 lYProProGlyAlaAlaGlyProAlaGlyPro 950
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Search completed: May 7, 2003, 15:27:03
Job time : 122 secs